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day of January 1999

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Patents Act 1990

CSL LIMITED

PROVISIONAL SPECIFICATION

Invention Title:

Porphyromonas gingivalis probes and polypeptides

The invention is described in the following statement:

Porphyromonas gingivalis probes and polypeptides

FIELD OF THE INVENTION

5 The present invention relates to *P. gingivalis* nucleotide sequences, *P. gingivalis* polypeptides and probes for detection of *P. gingivalis*.

BACKGROUND OF THE INVENTION

10 Periodontal diseases are bacterial-associated inflammatory diseases of the supporting tissues of the teeth and range from the relatively mild form of gingivitis, the non-specific, reversible inflammation of gingival tissue to the more aggressive forms of periodontitis which are characterised by the destruction of the tooth's supporting structures. Periodontitis is associated
15 with a subgingival infection of a consortium of specific Gram-negative bacteria that leads to the destruction of the periodontium and is a major public health problem. One bacterium that has attracted considerable interest is *P. gingivalis* as the recovery of this microorganism from adult periodontitis lesions can be up to 50% of the subgingival anaerobically cultivable flora, whereas *P. gingivalis* is rarely recovered, and then in low
20 numbers, from healthy sites. A proportional increase in the level of *P. gingivalis* in subgingival plaque has been associated with an increased severity of periodontitis and eradication of the microorganism from the cultivable subgingival microbial population is accompanied by resolution of
25 the disease. The progression of periodontitis lesions in non-human primates has been demonstrated with the subgingival implantation of *P. gingivalis*. These findings in both animals and humans suggest a major role for *P. gingivalis* in the development of adult periodontitis.

30 *P. gingivalis* is a black-pigmented, anaerobic, asaccharolytic, proteolytic Gram-negative rod that obtains energy from the metabolism of specific amino acids. The microorganism has an absolute growth requirement for iron, preferentially in the form of haeme or its Fe(III) oxidation product haemin and when grown under conditions of excess haemin is highly virulent in experimental animals. A number of virulence factors have been implicated in the pathogenicity of *P. gingivalis* including the capsule, adhesins, cytotoxins and extracellular hydrolytic enzymes.

In order to develop an efficacious and safe vaccine to prevent *P. gingivalis* colonisation it is necessary to identify and produce antigens that are involved in virulence that have utility as immunogens to generate neutralising antibodies. Whilst it is possible to attempt to isolate antigens 5 directly from cultures of *P. gingivalis* this is often difficult. For example as mentioned above, *P. gingivalis* is a strict anaerobe and can be difficult to isolate and grow. It is also known that, for a number of organisms, when cultured *in vitro* that many virulence genes are down regulated and the encoded proteins are no longer expressed. If conventional chemistry 10 techniques were applied to purify vaccine candidates potentially important (protective) molecules may not be identified. With DNA sequencing, as the gene is present (but not transcribed) even when the organism is grown *in vitro* it can be identified, cloned and produced as a recombinant DNA protein. Similarly, a protective antigen or therapeutic target may be 15 transiently expressed by the organism *in vitro* or produced in low levels making the identification of these molecules extremely difficult by conventional methods.

With serological identification of therapeutic targets one is limited to those responses which are detectable using standard methods such as 20 Western Blotting or ELISA. The limitation here is the both the level of response that is generated by the animal or human and determining whether this response is protective, damaging or irrelevant. No such limitation is present with a sequencing approach to the identification of potential therapeutic or prophylactic targets.

25 It is also well known that *P. gingivalis* produces a range of broadly active proteases (University of Melbourne International Patent Application No PCT /AU 96/00673, US Patent Nos 5,475,097 and 5,523,390), which make the identification of intact proteins difficult because of their degradation by these proteases.

30

SUMMARY OF THE INVENTION

The present inventors have attempted to isolate *P. gingivalis* 35 nucleotide sequences which can be used for recombinant production of *P. gingivalis* polypeptides and to develop nucleotide probes specific for *P. gingivalis*. The DNA sequences listed below have been selected from a

large number of *P. gingivalis* sequences according to their indicative potential as vaccine candidates. This intuitive step involved comparison of the deduced protein sequence from the *P. gingivalis* DNA sequences to the known protein sequence databases. Some of the characteristics used to

5 select useful vaccine candidates include; the expected cellular location, such as outer membrane proteins or secreted proteins, particular functional activities of similar proteins such as those with an enzymatic or proteolytic activity, proteins involved in essential metabolic pathways that when inactivated or blocked may be deleterious or lethal to the organism, proteins

10 that might be expected to play a role in the pathogenesis of the organism eg. red cell lysis, cell agglutination or cell receptors and proteins which are paralogues to proteins with proven vaccine efficacy. DNA sequences that were considered to be poor vaccine candidates and not selected include those that code for proteins involved in replication, non-essential proteins

15 involved in cellular processes and those proteins present at sites that would be unlikely to be affected by immune mediators such as those found in the bacterial cytoplasm or inner membranes.

In a first aspect the present invention consists in an isolated *P. gingivalis* nucleotide sequence, the nucleotide sequence consisting of or

20 including a sequence selected from the group consisting of SEQ ID NO: 1, SEQ ID NO: 2, SEQ ID NO: 3, SEQ ID NO: 4, SEQ ID NO: 5, SEQ ID NO: 6, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 10, SEQ ID NO: 11, SEQ ID NO: 12, SEQ ID NO: 13, SEQ ID NO: 14, SEQ ID NO: 15, SEQ ID NO: 16, SEQ ID NO: 17, SEQ ID NO: 18, SEQ ID NO: 19, SEQ ID NO: 20, SEQ ID NO: 21, SEQ ID NO: 22, SEQ ID NO: 23, SEQ ID NO: 24, SEQ ID NO: 25,

25 SEQ ID NO: 26, SEQ ID NO: 27, SEQ ID NO: 28, SEQ ID NO: 29, SEQ ID NO: 30, SEQ ID NO: 31, SEQ ID NO: 32, SEQ ID NO: 33, SEQ ID NO: 34, SEQ ID NO: 35, SEQ ID NO: 36, SEQ ID NO: 37 and sequences complementary thereto.

30 In a second aspect the present invention consists in an isolated *P. gingivalis* polypeptide, the polypeptide being at least partially encoded by a nucleotide consisting of or including a sequence selected from the group consisting of SEQ ID NO: 1, SEQ ID NO: 2, SEQ ID NO: 3, SEQ ID NO: 4, SEQ ID NO: 5, SEQ ID NO: 6, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 10, SEQ ID NO: 11, SEQ ID NO: 12, SEQ ID NO: 13, SEQ ID NO: 14, SEQ ID NO: 15, SEQ ID NO: 16, SEQ ID NO: 17, SEQ ID NO: 18, SEQ ID NO: 19, SEQ ID

NO: 20, SEQ ID NO: 21, SEQ ID NO: 22, SEQ ID NO: 23, SEQ ID NO: 24, SEQ ID NO: 25, SEQ ID NO: 26, SEQ ID NO: 27, SEQ ID NO: 28, SEQ ID NO: 29, SEQ ID NO: 30, SEQ ID NO: 31, SEQ ID NO: 32, SEQ ID NO: 33, SEQ ID NO: 34, SEQ ID NO: 35, SEQ ID NO: 36, SEQ ID NO: 37 and sequences
5 complementary thereto.

In a third aspect the present invention consists in a nucleotide probe specific for *P. gingivalis*, the probe including a detectable label and a nucleotide sequence of at least 15 nucleotides, the nucleotide sequence being derived from a sequence selected from the group consisting of SEQ ID 10 NO: 1, SEQ ID NO: 2, SEQ ID NO: 3, SEQ ID NO: 4, SEQ ID NO: 5, SEQ ID NO: 6, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 10, SEQ ID NO: 11, SEQ ID NO: 12, SEQ ID NO: 13, SEQ ID NO: 14, SEQ ID NO: 15, SEQ ID NO: 16, SEQ ID NO: 17, SEQ ID NO: 18, SEQ ID NO: 19, SEQ ID NO: 20, SEQ ID NO: 21, SEQ ID NO: 22, SEQ ID NO: 23, SEQ ID NO: 24, SEQ ID NO: 25, 15 SEQ ID NO: 26, SEQ ID NO: 27, SEQ ID NO: 28, SEQ ID NO: 29, SEQ ID NO: 30, SEQ ID NO: 31, SEQ ID NO: 32, SEQ ID NO: 33, SEQ ID NO: 34, SEQ ID NO: 35, SEQ ID NO: 36, SEQ ID NO: 37 and sequences complementary thereto.

20 Throughout this specification, unless the context requires otherwise, the word "comprise", or variations such as "comprises" or "comprising", will be understood to imply the inclusion of a stated element or integer or group of elements or integers but not the exclusion of any other element or integer or group of elements or integers.

25

DETAILED DESCRIPTION

Preparation of the *P. gingivalis* library for sequencing.

30 To determine the DNA sequence of *P. gingivalis* genomic DNA was isolated from *P. gingivalis* strain W50 (ATCC 53978) essentially by the method described by Mamur J. (1961). Cloning of DNA fragments was performed essentially as described by Fleischmann *et al.*, (1995). Briefly, purified genomic DNA from *P. gingivalis* was nebulized to fragment the DNA and 35 was treated with Bal31 nuclease to create blunt ends then run twice on preparative 1% agarose gels. DNA fragments of 1.6-2.0 kb were excised from

the gel and the DNA recovered. This DNA was then ligated to the vector pUC18 (*Sma*I digested and dephosphorylated; Pharmacia) and electrophoresed on a 1% agarose preparative gel. The fragment comprising linear vector plus one insert was excised, purified and this process repeated 5 to reduce any vector without insert contamination. The recovered vector plus insert DNA was blunt-ended with T4 DNA polymerase, then a final ligation to produce circular DNA was performed. Aliquots of *Epicurian Coli* Electroporation-Competent Cells (Stratagene) were transformed with the library DNA and plated out on SOB agar antibiotic diffusion plates 10 containing X-gal and incubated at 37°C overnight. Colonies with inserts appeared white and those without inserts (vector alone) appeared blue. Plates were stored at 4°C until the white clones were picked and expanded for the extraction of plasmid DNA for sequencing.

15 **DNA sequencing**

Plasmid DNA was prepared by picking bacterial colonies into 1.5ml of LB, TB or SOB broth supplemented with 50-100ug/ml Ampicillin in 96 deep well plates. Plasmid DNA was isolated using the QIAprep Spin or QIAprep 96 Turbo miniprep kits (QIAGEN GmbH, Germany). DNA was eluted into a 20 96 well gridded array and stored at -20C.

Sequencing reactions were performed using ABI PRISM Dye Terminator and ABI PRISM BIGDye Terminator Cycle Sequencing Ready Reaction kits with AmpliTaq DNA polymerase FS (PE Applied Biosystems, Foster City, CA) using the M13 Universal forward and reverse sequencing 25 primers. Sequence reactions were conducted on either a Perkin-Elmer GeneAmp 9700 (PE Applied Biosystems) or Hybaid PCR Express (Hybaid, UK) thermal cyclers. Sequencing reactions were analysed on ABI PRISM 377 DNA sequencers (PE Applied Biosystems).

The sequences obtained are set out below.

30

DNA sequence analysis

Raw trace data files from the ABI 377 sequencer were manually 35 trimmed using Staden Pregap (Laboratory of Molecular Biology, Medical Research Council, UK) running on a Sun Microsystem computer. Trimmed files were assembled into contigs using Staden Gap v4.1 and exported as a consensus file in FastA format. This consensus was converted into GCG

format files and analysed for homology using the FASTX algorithm on a non-redundant protein database compiled by ANGIS (Australian Genomic Information Service, University of Sydney). Individual FASTX search results were examined for significant homology by statistical probability and 5 amino acid alignments.

The results are set out in Table 1.

It will be appreciated by persons skilled in the art that numerous variations and/or modifications may be made to the invention as shown in 10 the specific embodiments without departing from the spirit or scope of the invention as broadly described. The present embodiments are, therefore, to be considered in all respects as illustrative and not restrictive.

Dated this 9th day of March 1998

CSL LIMITED

Patent Attorneys for the Applicant:
F.B. RICE & CO.

References.

Mamur, J. (1961) A procedure for the isolation of deoxyribonucleic acid from micro-organisms. *J. Mol. Biol.* 3, 208-218.

Fleishmann, R.D. et al. (1995) Whole genome random sequencing and assembly of *Haemophilus influenzae* Rd. *Science* 269, 496-512.

Table 1

Contig #	SEQ ID	Homology description	Accession number	% identity	Overlap (aa)	Statistical expectation
1363	1	Outer membrane integrity protein, <i>Haemophilus influenzae</i>	P71397	38.3	269	5.30E-34
1448	2	Outer membrane protein P64K or PM-6, <i>Neisseria meningitidis</i>	Q51189	44.8	116	1.20E-14
1506	3	Heat shock protein HTPG, <i>Actinobacillus actinomycetemcomitans</i>	G862902	34.3	458	1.40E-50
1534	4	HemB, <i>Porphyromonas gingivalis</i>	P95494	33.6	116	2.00E-11
1976	5	Zinc protease, <i>Escherichia coli</i>	G535004	28.3	272	9.30E-21
2073	6	Membrane fusion protein mtrC, <i>Haemophilus influenzae</i>	G64100	23.6	152	7.00E-07
2080	7	Outer membrane protein A, <i>Escherichia fergusonii</i>	G146991	52.5	59	1.30E-08
2152	8	Heat shock protein HSLU, <i>Haemophilus influenzae</i>	U32731	45	111	3.20E-14
2159	9	63kD protein, <i>Bacteroides gingivalis</i>	AB004560	32	382	5.50E-48
2307	10	Adhesin protein, <i>Synechocystis</i> sp.	D90903	30.1	229	5.00E-10
2389	11	Internalin A, <i>Listeria monocytogenes</i>	M67471	40.1	212	2.50E-21
238	12	Outer membrane protein X precursor, <i>Vibrio cholerae</i>	Q07023	29.1	172	5.30E-05
2425	13	Amylovoran export outer membrane protein AMSH, <i>Erwinia amylovora</i>	G600428	34.4	151	6.10E-06
2802	14	Outer membrane protein MIP, <i>Legionella oakridgensis</i>	G2231734	49.8	201	6.50E-37
2847	15	Hemin permease, <i>Yersinia enterocolitica</i>	G541768	32.6	141	3.20E-12
3064	16	Protease, <i>Helicobacter pylori</i>	G2314520	29.2	144	1.10E-11
3093	17	Thiol protease/hemagglutinin prfT precursor, <i>Porphyromonas gingivalis</i>	M8309	24.9	225	6.90E-09
3300	18	Hemolysin, <i>Synechocystis</i> sp.	D90914	22.6	283	1.30E-10

Table 1
(cont.)

Contig #	SEQ ID	Homology description	NO.	Accession number	% identity	Overlap (aa)	Statistical expectation
3589	19	Hemolysin A, <i>Prevotella melaninogenica</i>		U27587	64.2	67	4.50E-15
3655	20	Internalin A, <i>Lysteria monocytogenes</i>		M67471	39.3	300	1.10E-34
3772	21	Heme uptake protein A, <i>Bacteroides fragilis</i>		X97122	85.3	224	2.60E-90
3782	22	Arg-gingipain-1 proteinase, <i>Porphyromonas gingivalis</i>		U15282	39.9	143	1.40E-15
4041	23	Trypsin-like protease prtT, <i>Porphyromonas gingivalis</i>		A49228	69.2	39	8.50E-04
4174	24	36kD antigen, <i>Helicobacter pylori</i>		U86610	36.4	162	2.70E-19
4188	25	Polar flagellar protein, <i>Vibrio parahaemolyticus</i>		U12816	41.1	175	9.10E-18
4216	26	Trypsin-like protease prtT, <i>Porphyromonas gingivalis</i>		A49228	53	68	1.10E-06
4381	27	Hemagglutinin, <i>Prevotella intermedia</i>		AF017417	50	186	9.80E-33
4381	27	Abortive phage resist. Protein, <i>Lactococcus lactis</i>		U94520	39.5	124	8.00E-12
4413	28	DNA K heat shock protein, <i>Borrelia burgdorferi</i>		M96847	67.8	233	1.10E-68
4424	29	Heme A uptake protein, <i>Bacteroides fragilis</i>		X97122	69.9	171	8.20E-47
4426	30	36kD antigen, <i>Helicobacter pylori</i>		U86610	38.1	110	8.20E-11
4457	31	Outer membrane protein P4 precursor, <i>Haemophilus influenzae</i>		A43604	33.9	254	5.00E-23
4538	32	Polar flagellar protein, <i>Vibrio parahaemolyticus</i>		U12816	50.6	218	3.50E-44
4729	33	Outer membrane protein P64K or PM-6, <i>Neisseria meningitidis</i>		X84696	32	200	7.10E-15
4763	34	Hemolysin or CLPB protein, <i>Serpulina hyodysenteriae</i>		X73140	59.3	145	1.90E-24
496	35	Hemolysin, <i>Serpulina hyodysenteriae</i>		Q54318	37.8	156	3.50E-21
723	36	Protease, <i>Helicobacter pylori</i>		G2314520	46.7	139	7.40E-22
933	37	Hemolysin or CLPB protein, <i>Serpulina hyodysenteriae</i>		Q54316	47.7	388	3.70E-75

'2) INFORMATION FOR SEQ ID NO:1

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 885 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...885
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1

cgccggagga	ttcgtatcat	ctaataatcca	ctcatctgtg	tcgggtaagt	gctgaagatc	60
gataacgtat	acgactcaag	cgctatccc	aagcccggt	cttcattagc	gtagaagggtg	120
acgaatggga	agaggcatac	gtcgctacc	agccatcg	aaagaatgca	atctggatgc	180
aaaagaaaatc	gtagccaaat	ttctgcagcc	cggatttgc	gttctggcg	gtgc	240
ccctaccatg	tgaagctgtc	ccctccctccg	ggcaacaaag	ctgagatct	gatctcaacg	300
cccttagatg	cgagccttat	ctgacgagcg	accatgtc	tatctggagc	acggcgaaga	360
gatcatgatc	ggcgtgagta	tctgtatgaa	agcatcagg	taaacaaggc	cgtcatcgga	420
gttggagaata	ataagaaaga	tctattgctc	acctcacaa	actggccact	gcatatccgg	480
gcatacgggt	atgcgttga	agtgcaata	tcctcaaggc	ggtgagaagc	agctgatcgt	540
gcgtatgtcc	gcaagcagg	aaaaagcggt	gccttgcc	ttagcacagt	gccgtagtac	600
aaaaacgtggg	tacggattc	gccgtgtac	aagcagttag	aagaacaagc	ctctggtcga	660
gcgcacgtgt	acggttacag	aaaaaaactg	tctcgccgt	ctaaccctct	cgttcgatata	720
ggtaactcc	ttgcgtttt	atcgaagcag	caggtggctt	gccggagaat	acgggcaaga	780
tcatggcgga	ggtccgatga	tggaccgc	ctctgtgtc	accggatgt	ccttgacc	840
aggcagctcc	ggagtattga	ttcttcgata	gagaagaggc	agtcg		885

(2) INFORMATION FOR SEQ ID NO:2

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 548 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...548
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2

ctggggaaaa	catgacgaaa	cgatgagcta	ccgtggcgta	ccaggtgtgt	gtacaccaat	60
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ctgttcgtcg	ccttcctatg	gccttctcg	tcgatttgc	gcagaaaacg	aacaaggcaa	180
tggagagtgc	aaactatact	tgtatgaaag	aaccgcttga	tcggagcaca	cctcattggc	240

atccggcgg cgaactcatc gtaaccgctg ccatggccat cgagaccggc atgaggatcg	300
acaaatcgaa cgaatcatat tccctcatcc gactgttaggc gaatcctaaa agaaactctc	360
ccggagggtt gatactttt ctggcccttt ctagggaaatc aaatctaaaa agtccgtgca	420
gtcaacaaaa actgcacgga ctttcctct cttaatatct tttctcaga gtattcggag	480
taccccgaa gacagcaccc gaaaaacgag acctttggaa aataaggaga tggaggaaaa	540
gacttaaa	548

(2) INFORMATION FOR SEQ ID NO:3

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2309 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...2309

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3

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atccgtccgc gaattcaaag gcgagacggt gaccccgccg taacggctcg cgtggatgaa	180
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caaatactgt aagtccctta ccgtggccat cattttcgcc aagaagcaga atgaaagac	600
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caccgatatg gacggacaca agtacacgtt cgacgatacc gaacgctcg cgaaggtgt	1200
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gccacgtgaa acgtcatccg acaaaggcta cagcgtgtatc ctgttggat gtcagttgg	1320
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aattcatggc cgtatcgccg atatggcaca gtcgtggccg ggaatgagct tctacggaa	1620
ctccccgatt cgtacaatct ggtacttaat accgatcatc cgctcacgac agggtaactct	1680
ccgggtggaa agaatcggtt gggccctcg tcacaagctt agagcgaaaa tcgcccagct	1740
gaaagcggaa gggcccaacg tgctgtatc gaaaaaggaa agaaaccggg gggaaatccct	1800
gttggccacga aggacccaaat gagaacaacg ccgtcgaaaca ggcggaaaacc gaaggcagta	1860
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gctctgtcg gaagcggatt gctgacggg gaggcttgg cgaatttatt cgtcgacggcc	1980
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tgccaaataga catggcaaga gaggatggat ataatacaag gaaccccgaa aagccacggc	2100
tttcgggggt tgctttatc agagcttccg ccgtctctt ttccctcgta gaatgggtggc	2160
cgggaaaaat gcttacaatc cgaagatcg aatgaaaaga tagacggccg gaatacgaag	2220

gagcactgt ccagccggc cagtataacct ccattccggg aatgatatgg ccggaatcct
 tcactcctgc attgcgtttg agatggact 2280
 2309

(2) INFORMATION FOR SEQ ID NO:4

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 592 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...592
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4

gcacatttcc gctgaagcta agattgttag ttgcataata ggaaagcgat ggcttacacc	60
ctgattttcc tggcacgaa aagttttctt atacgtttctt ccaagaccgg ttgcggat	120
cctttttctt tttttatttc gaacggatat tctgccagcc atccgtatgg tagaagaaat	180
agttggatt gctactaact taccgatgtt tatatcgagc gaagtattgg tttgccgatc	240
gttgtttcg atatgcgtatg tgacgtatat gcactcgttc gattcgtatttcttgtga	300
tcacattgtat taccggcg atggcatcgg atccgtatag cgaactcgaag caccttcac	360
cagttcgatc cgttcgatct gatcaggaga aaacgactca aatcgccctg accgcctaca	420
tcggcgatca cagcgttacc acgataagga tgaggatata cttactgcta aggcgcntca	480
gctgcgttacaa gagcccatca gattggggcc gaagtcaaaa gacggactca gcccgtcata	540
ggcctcgaa gtaggagccg agaaaagaggc tatgtcctta gcggtaagac tt	592

(2) INFORMATION FOR SEQ ID NO:5

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 969 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...969
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5

gggttaacgac agcattttcc accggatcga tcattttggc aatagcctgt tgaatgcttc	60
cagaggaacc tgaggagcaa aagcattcac cgtctgattt ccacctaatt acccggtata	120
tagccgcattt cggtaagta ggtggagatt cattggata agcattgttc ttacgcttgt	180
ctctttcggtt gtattgttct cgtatcgctt gaggcacattc gngccgtgca cgatccgtat	240
tcgccttgggtt gaataccgaa ctgacggagg ctttctatct ctgcccaccaa tgcgtcatcg	300
ctttctccgc ttcaccctca cgaaccgagg caacaaaattt gaagcgtcct tagtctgggt	360

atgtacatg aagttagaga agaaagctcc tgactgagga aaggagcggtt aggcttgtga	420
qtaatctcg acagacgctc atcacggctg tagtgatcac ctgtttcata tagtcttcca	480
aagtccgaa atcgatcctc gcacttcttgg aggagtgggg tcgctcttga agctgatggg	540
agctgcgtgg tagtagcctc agcatcggtt gcaatggctt cgataggccatcgatgggg	600
ctaccggcgat atagatacgc tctgtggat tcacggggca ggaacgtcct tgaagagtcc	660
tttgatcttgc ttctccacat agtccaaatcg atatctccca cgatcaccag accttgcagg	720
tcgggacgat accattctta taatagttgc gcagctcatc atgcttgaag ttgagcacga	780
cgtcatcaga ccgatgggca tgcgttctgc atatttattt cccggcatacg cctggcaagt	840
atagcctcga acatacgaag gttggcatcg cgacgacac gcaacttcc tggatcacac	900
cgcgctcctc gtcgatctca tgcccgtcga ggtaatattt ttactccaaat catgcaggat	960
aagcaagcg	969

(2) INFORMATION FOR SEQ ID NO:6

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 729 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...729

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6

cgaagaagat ctgcaagccg gcgaggacta ccaatatgcc gtggagggcg caggctcgatcg	60
atggaacggc agcggcgatgg ttcgtctcac agggggatca ggtgcggcag atggaggaga	120
gcctccataa tatgcgtcg aatctggat ggtgcgcgc cgtgtggaa acctgaacgt	180
gaaggcaccg gccgacgtca gttggggctt ttggacgtgg agataggcgac gacggtagga	240
gcggcgatcg catcgacag atcaacgtcc tgcgtccacta caaggtggag gctagataga	300
cgagcactat atcgatcgatcg tcaaaagccgg tctggccgt tcgtcgaaacg gcagggcagg	360
gacttctccc ttgcgttcg gaaggtatac ccgaagttcg ggacaagcag ttccgcaccg	420
acttcatatt cgacggagag caccgcacaa tatccgcaca ggccaaactt actacatcaa	480
tctgcgcctc gacagccgtc cgaagccatc atgatcccgc gcggagcctt ctatcagaaa	540
ccggcgacg atggatattt gtcgttacgc ccgacggcaa gcgagccgtc gccgggacat	600
cacgattgccc cgtcagaatc cgacgttccat cgaagttccat ccggcctgca ttggcgncga	660
gatggtcatc acctttcgta tgatattccg cgatgcataa gaaattatcc tgaatgaccc	720
acctatacg	729

(2) INFORMATION FOR SEQ ID NO:7

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 500 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...500

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7

gattttctg aaaccactag tagattttc tgaaactaat atcagattca cgtactgaaa	60
attaagtct tatcaaagca cacttggta ggcttgacg ctctacttt cattccacga	120
gcgattaacg caactcttct tcgatcaacg gaactcgta cgacggttca gttggtcgca	180
gactgactgc tgctcccggt caaaggtgct acgaattcct cggtagcac atgccttcc	240
ttcagaaatc gtgcccgtcg gcaattttgg ctgtcaccgt cttggggaca gactaccgt	300
gccttccac gtaaggctgt cggccgctat gccacgactc gtgggtaatc caccacggat	360
ttggctctgc ggtcagatag tccgaggttg tagcatcggg gccttcctg tcggcatgca	420
aacccaattc gatccgata tccgattgtc cgtgaggata cgaaatcagt tcgtccaagc	480
tcttcatgct ttcggcgaa	500

(2) INFORMATION FOR SEQ ID NO:8

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1169 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1169

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8

ttcgcccatt gacatcacgc gtaatcgaag gattatcaact cttacggca tcttgtctat	60
ctcatcgata aagacaatcc ctctctcgcc ctgttgaat ctagtctgc ggcctgcaaa	120
agtctggta gaatactctc aatgtctccc ccacatagcc ggcttcggtc agtacccgt	180
cgtcactac ggcgaaggaa catggagcat tttggctatac gtacgagcca agagtgtctt	240
gccggtcccg tgggaccgac cataataata ttgctttct ctagtctctac gccacgctgt	300
cctcttgcg gagcaatcgt ttgtatgat tgtatacagc gacgaaagaaa aacgtttggc	360
atcatcctgc ccgataacat acgaatcggag aattccttga tctctatagg ccgaggcaag	420
tcctctctc tcagattttt ctctcttccg atttgaattt ttgcaatgct tctcgaaccca	480
cctctcctgc cggagagac attcatacgca gatatgagca tgactccct cgagcatcg	540
tttacctgcg ttctcgccat gccacaaaaa ctacagtatt ctctgtccct ttcttgcca	600
tgagaaatat acagtccccc tttggtaac gagagggtac ttgcattct ttgcaggat	660
tttatctatc atcccgtaact ccaatgttgc ggggctgtca tccaatagtc ccgatacta	720
tctttttcga cctggcggacg ggcttccac tttggaaaga gataatcgtaaaagcttctt	780
tcttacgcgc agaatctcgc gagctgcgtat ctccaaatcg ctggcctgccc cctcatacca	840
ccaaagcggct gatgtatcat cacggggaa tgaggcaag caagcggttgc ctttcgttc	900
ctgctacgag cagcactgat gccatagacg cgccatgccc gtacagatag tggccacatc	960
gcaccctata tactgcacatc atcgatatacg ccataaccgg cataaaacaga tccgcgggt	1020
gaattcagaa gatggaaata tctttaccgg ggtcggcgct atcaagataa agaagctggc	1080
ttgaatgaca ttggccgtgt aatcgatcgat ctgagtgcca aggaagagat ccgatccatc	1140
attagacgtg agaacacatc catttgc	1169

(2) INFORMATION FOR SEQ ID NO:9

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1144 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1144

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9

cgttacactt tcagggaaat acttaagggt cgtattcaga gcaaacaag ctcttggc	60
ccctcaggat aagacattgc cacacggta atttcggctc actaagtctt ttcggagcag	120
tcttaatgtat ttcacgagct tcttcgaggt ataatcacga acgatataacc ccatggttat	180
cgtattgcga cgaaatccgg atagatctga tccaaagatata aacgataaga cgaaagggtgc	240
ttcaggcctg ttcacgtgca tcatacatcg catatttatac ggagttgatt atctcaatac	300
gccccacgta tcggctatata cactctttc gatagccagt ttcgccccctt ccaatcttca	360
ccgcccattt cagtggttat attcggcaat gtttgcata cttacgcacc aattcttccg	420
cgagtctttt agcacggcgc tcgacaaagc cttattgtgg gctattgaag cctcgggaga	480
agcaaaaccctt cgatgtatcat ttatttgacc gaatagttt gattagcctt aacgggtcta	540
caaattctttt gattttctt aactccgcctt atttttgccg atactcagaa ggacatctgc	600
cttatttgact ttgaagttga tataaggcatc gaagctgact ctcgctgttt ttccacttct	660
tctgcccggat taatgtgtgc cancaataag gagcctctgc cggattgaag agtggatcaa	720
aaggancaatt attaccgaga gacctacagg gcatttagca caacctcgta cctcctcagc	780
aaccccaactt tggcatccat catccatgtat gcataagcat gttctccgtt aaagcaaaact	840
gctcgctttt cccattatga cggcgaatgtt atttagctgc atttttgcattt gggccaaagc	900
cgaactaaat gcgatttcac gcttgagagc ttgttctat tgcggccgtt aatgactacc	960
gaaggaaattt ccacccggctt gtaccatctt ctgaacgaag aataggcgtt acaatgatca	1020
tctgagtgcc ttgagcttta aattactcat atctgcccga ccattcagta caaccttgc	1080
ccggttttgtt ccaacgaaat ttatatgaa attactccctt cgtaagcttt tgagcgttca	1140
aacc	1144

(2) INFORMATION FOR SEQ ID NO:10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 719 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...719

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10

cctttttttt acgattttcc cggccttcat cctcggcgct actgctttgc ggcttggaa	60
gggggtactg ttccaggctc cgatcgta cttggctgtac catcgagcca cagaaataact	120
tcatcgagtc cattgcggat aagtccggca ggtgggtggca ttggtaccgg cccgcagcaa	180
tccggaggaa tacgacccctc gcctaccgtt atgaagcggtt tgccgaagc agatgcctac	240
ttctaataagg aggactgggg ttccgagcaaa gaaatctcgc tgccattcgg gacataacc	300
taagctccctt cttttcgaaa tggcggat gccgaagtgc agatctccac	360

gctcctgca cagatcattc tcatacagac ctcatgccc	tgatccgac tattggagca	420
gtgtggtagg ggaaaggca ccagtcgtgc tgcatacgc	gcccgttgg agctttatcc	480
aacgagaaa acaaattggc acaaaggcac gaccgtctca	acggacgtat cgacagcgta	540
agagactcg tgcataccatg tttgccaatg gcaaagcaga	caaagcctcg tcatatatca	600
cccatcgntc agcttttcg cccaagagtt cggcctggc	agatcgcat agaggaagat	660
gggaaagagc ctacggctgc ccacctcgtc gtgtggatcg	atcaggcacc gtgccatg	719

(2) INFORMATION FOR SEQ ID NO:11

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2437 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...2437

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11

agattcagga tgctcgctat ctgttggtat tcaaatgtac	caaaccncnt atccgcaatc	60
ggatcaccacc ggaatcaata accagaaaaac atataatttg	agtgtacacg acattatcg	120
tgacgaaagg gttactatcg tacaagggtt aacggcatcc	tgctgtgtca ggaatcggtgg	180
atggcaggca aaagcccaaa tgggaccgaa accatccaa	cgcgatttgc gacacggaaag	240
ccgatggccg agctcaatg aacgagatc ggacaataaa	accacccctt aaaagtatgc	300
aaaccatcat caccacattc atccctttat ttagcttgc	gaatgtctc cctcttctat	360
tccatcttca acgagaagcg actgtacgc aaggcgcagt	acatgttgc aagctcaatt	420
cgctttcct caccctggct ccatagccta ttacttact	ttccctgtacg aagcttatgc	480
cacgggagtc agttcaatac gctatccggc	ttggggctgt cgatcttgg	540
ccatgctctt ttgcgtcatac tataagctga	ttttgcctag gggatgtgt	600
acccgatcat cgtatcgaaa cgagttcct	gacgcgtgac tctatatcg	660
ctcaacgtca ttccggagct tatcgatca	ttcccttttgc caatgttgg	720
gtgtcgaaat gcccgtatc tcgctatcct	tttcgttgcg atccgtcagg	780
catgagcattc tatggggcgc ggtacgatac	aaagagcgc	840
cagaccgaaa aagtttcaa caacgaagac	agaatgattt tggcaaaaaa	900
aaggaaaggag atcctgaatg aaaaaaagcag	ggctaaaata	960
tttcaaactc tttgcaaaac	tttttcgat	1020
ttcgaaaaatcataaattcgt ttccatttg	tttgcattat	1080
cgacggctc aaaaggccca ttcccgagct	tttgcattat	1140
acgaatcggat tgcgtgcctt atctgtttgc	tttgcattat	1200
tcatacgccc tgcgttgcctt ctttgcataa	tttgcattat	1260
cgatctgtcc gggtcgttgg tgcgttgc	tttgcattat	1320
gtcttcgtt atgcgttgc	tttgcattat	1380
gtggagctt ctcggctt caaatgttagc	tttgcattat	1440
ttttggagaa caatcttgc	tttgcattat	1500
cttgatttgt aatgcgttgc	tttgcattat	1560
tactcacaca ttgatggaaa tttatggggca	tttgcattat	1620
ttttccttgc ttgcgttgc	tttgcattat	1680
gatatgacaa ccaagaaacc ccaagccatt	tttgcattat	1740
ttcctgtatc tccctcacaa gaaggataag	tttgcattat	1800
ttcctccggc gcatcggttgc	tttgcattat	1860
ctattgattt tcctgcgtca aaaaagctt	tttgcattat	1920
gggtctagaa cgttactt cgttacaaa	tttgcattat	1980
ctagagggcc tggatagtct cacctcgta	tttgcattat	2040
gtaagctaga gggctggac gtcaccc	tttgcattat	2100
aatcgtaac tagagggtct ggaacgttcc	tttgcattat	2160
accaaatacg taagctagag ggtctggaaac	tttgcattat	2220

agtaaccag atcagtaaac tagagggcct ggatgtctca cctcgctaac aaaactttct	2280
ctctccgata accaaatcg taactagagg gtctggAACg ttcacccctcg ttagcggagc	2340
ttatctttt ggtaaccaaa tccgtaagct ggagggctcg gaacgtctca cgtccttagc	2400
acgcttgaac tattcggtaa ccaaattccgt aagctgg	2437

(2) INFORMATION FOR SEQ ID NO:12

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1626 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1626
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12

gagggctttt attcataatt cgctcagata taaaacgaga gtttaattcag tagccgattt	60
cgacgaatag tttcttccaa cattcataga tatttgcga gaggtagatt tgaccatcaa	120
ctctgattct tgtcccatatt tcttacgaga gtttcatcat ccatcaataa gcgttaactta	180
tccgcgaagt cttcatgtct tccatggca caaggaaacc attgcgaccg tttcgatca	240
gttcctcggg ccggtcggac aatcgatcg gatttaggt agtgcataatg cttcgcttcg	300
agaagtagcca ttggtagtcc ttgcggaaacgg gacgtcatta gataatagca gatgattccg	360
tagtatttgc gaatttccgg ttagatggg attatttcta tttgcgactc catattgcga	420
gatgcaattt ctttacgtat ctcgattcat tttcgccatc tccgactatg ataagcttcc	480
aatcaggcct ttcgcgcgca ctcgtatgc atcttctatc atgaattcaa aacccttctg	540
taggttaagc ctgccaatcg ccaacatttgc tttgtagta gtagcatcct ttggactgta	600
gttaatggaaa cttgattggg tatgacatat gctttaggcg tccacgtaaatg attgcctcga	660
acgattgtcg atctttttt gtcagtctac aacggcatca agccctgaat acagaaaccc	720
ccttatgcgt tttgtataagg gcgggcaata tcataagaga tatgttcgca tccgatcgta	780
aatatctgcc tctgttactg atctgagaca aaattgtatt gataaaaata ttatccctat	840
caataaaacc ggttcacgt tcttgcata ggtttttatc ctcgataagc cttgaaatata	900
actgttttgc gggctaatgc attgcccataa acctaattcc gagatgggt acttctattc	960
cttttctac ttggaaaggaa gctctccctc ttttgcataa acgctgacta atgatacgcg	1020
atgaccatttgc catgcagggtt gtttagccaa ttgatcacgg cgcgttctgt accggcacgt	1080
ttgttattgt atctaacagc agataaaatca tagagaatat tttaacgttc ttttttaaga	1140
aattcatcaa ggctattggt agtattaata gcttcaatata tattgtatttgc aattcctatg	1200
tgaatctatt tcatttgatt gatatctggg taagcatgcg gtttgcgttgcgat cgcataatgc	1260
atattcagct gcaaaattcat gatttttttt gatattccaa agattcttttgc cgggatttg	1320
ccattgttgg tcatcttattt gtccttttgc gatgttttcg cccaaacctg ataaaatcat	1380
tccacccctgt tttttttttt atgtgcgattt aaaggataat gcttttcgat acctccttca	1440
ataggcaata acacggattt ctgagggtcgat ttcttgcata gctctttatc ggaggccata	1500
atgcactgg ttgtcgattt atatgcagaa tttaaggatcgat tgatcttct ttttccttgc	1560
aatatgcgattt cttcatgcct tttttatctc tttggcttgc aattctccctt tatgtttcgc	1620
aatacc	1626

(2) INFORMATION FOR SEQ ID NO:13

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 556 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)

- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...556
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13

gcaagatata	caaactttta	atcgggagat	tatcgctaaa	ccatatgact	aaaaatttag	60
aaggacgatg	tgctgaacat	ccttgcagc	agtagagacc	ggagcttca	acgcctaca	120
accaagtgtt	gaccactcgt	gcactggccg	caacggctat	ggaacgaact	cgaacgaagg	180
cttcctggtc	gattcgaagg	gtacatcaat	tatcctattt	taggcccagat	ctatgttagag	240
ggcctactcg	taccgaactg	gagaaggaga	tacagaagag	gattatttcc	agtgatttat	300
caaggatcct	acggtaacgg	tgcagcttca	aaatttcaag	gtgcggttt	gggagaggtg	360
aatcatccgg	gttcgatgtc	ggtaaaagga	gacgaataac	tcttttggaa	gcgatcgaa	420
tggccggaga	cctgacaatc	ttggtcgccc	gcgatcgggt	ttttgtgatt	agagaaaaccc	480
gatgggcattc	cgaggttttc	cagacggatc	tcagaaaggc	ccacttgctc	gcaagccct	540
gtactatctt	gcattc					556

(2) INFORMATION FOR SEQ ID NO:14

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1853 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1853
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14

caaggctatg	ctatcctttt	cactgacaac	cggtagtgtc	agcatttttt	tacagccgac	60
ggctcctaaa	gccaagaggg	ctgaggcgat	aattgcaatg	ttttttcat	ttggagtttc	120
ccttatgttt	tttacgtta	gttttctat	ttggagtagg	ttttgccggg	ataggctttg	180
ccggcttctc	tacgaaggct	tgatttcgag	tagttctact	tcgaagaaaa	gcgtagagtt	240
cggctgagaa	gttcgcccatt	gctacgttcg	ccatatccca	gttcggtcgg	gatacaaatt	300
cgtacttggc	acccttttgc	atcagacaaa	caccctcagt	ccacccggaa	tcacttgcag	360
gaggctgaac	tttgcggct	cgttgcgaga	atagagctgt	cgaattctt	cccttcaatg	420
ttcttgccca	cataatgaac	acgaccgtat	cctgaaccgt	cgggcgaggt	ccttccctt	480
ccttcaagac	cgataacaaca	aaccgctttc	ggtagcctta	acgcccggct	gcttgcgatt	540
tcttcctgat	aagctttgcc	tgctgccaag	ttttcggctt	tgagtctgcc	tgtacttcct	600
tgaagtattt	cttgatcatt	tcgtccgcat	tttgggagag	atagcagtgc	tcttcccat	660
gagtacttct	tcgaatgctc	ggagaacagg	gcacgatcca	gagaatcgcc	cgccatccgt	720
ccggatatgt	cattgaattt	attgctccgc	ttataccgaa	agcgtatgcc	acagagtca	780
cagagtca	ataggcttca	cggtttgcac	ctcatcctt	ttggcgggtt	ttttgcaaaag	840
gcagataatc	cggccactaa	aaaggctaag	ccggcaatga	tcttactctc	tccatagtga	900
tttgcgttct	gattatttgt	tgatactcaa	tattcgatta	taaaaatgag	cgtactaccc	960
ggttgtat	gttcgcccggc	ccacgatctc	catacgccag	atcgctcggt	atagttactt	1020
tccacttggt	cctacaggca	ttaattgaag	aatctccgtc	cagccggcta	taactccctt	1080
agagggaaac	tggccgggttc	ccccctgtcc	atagagctat	cgaaaacata	ccgttcat	1140

cgtaccgtg	ataatgacag	gttaccgtgt	ccgaaagggtg	ggtttcgggc	cctctcccat	1200
ttaatgact	tcgtattgca	agccgtcggt	aaggctgtca	cacccctt	gtgtgcattt	1260
tcttgagga	attctctccg	gcctcttgc	tcagttgac	agccttctgc	tgcaaatcca	1320
tgaatacgcc	tctatttcgc	gcttggcctc	gtcatacagag	agctgaggg	cttttcttcc	1380
agtacatcg	acagacccgt	catgaaatca	tccataaacga	cctgtcgatg	cccaagact	1440
tgaaattatt	accgatgtc	aatcccagag	atagctca	ttatccatgt	aacacttgct	1500
tagttctta	tatgcgcgca	aaatataaaat	tttacaccga	ttcctcatac	cggcacatgg	1560
caatatcttc	tgtgcacact	ccatcgccaa	ggcttgcgg	ttattcacag	attacgggtg	1620
catccatatac	gacactgttc	ctgtggcag	ctgtttattc	ggagccgtcg	attggcactg	1680
aagctgaaag	cgaaaagaaatg	aaaaatgaaa	aacctttgg	ggctggtccc	ccgaatgttt	1740
tttttatttc	caagccattc	gtatgtatct	gcacaccaat	tacatgaatg	gcgtgcttaa	1800
tttaatgct	ctctttatag	chacttataat	tttcgaaaaa	aagagctaaa	acg	1853

(2) INFORMATION FOR SEQ ID NO:15

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 416 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...416

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15

tgaatatagc	cgctgccgta	ggctcgctgg	cagtaatggg	gctgatcggtt	ttgtcagcac	60
caagggtgcgc	agccacgtta	cgctgctcat	tatccggcgt	tgatcgata	tgtagccact	120
gccgtcatcg	gggttattcaa	gttttcgt	tcgaagaaga	tattcggcga	tacgtaattt	180
gggggttggg	cagcttccc	gtgccacgga	ttcgcgaactg	agtttcttgc	ccattctgat	240
gttgacttta	ttccggccgg	tatgctcctt	gtcaagcagt	tgaatcttt	attgtgggag	300
aaagctacgc	acgtaatctg	gactgaata	ctcgtcgggc	acgctgtcg	tgatctttc	360
cggcggtttgc	ctcatcgct	ccggaacg	cttgcggcc	catcggttt	ttgggg	416

(2) INFORMATION FOR SEQ ID NO:16

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 705 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...705

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16

ggagaaaactc	gctcgaatga	aaccgc	aaaaa	ccaatttaat	gcgtcg	gccc	gggg	caacc	60		
gtcaggcg	atcgcg	tta	aaaat	ttta	gtctctt	tct	ctatgat	ttt	aatctctgac	120	
atatgaattc	gcactt	gttt	gataat	cggt	gtagcaatca	ttag	ctttag	atgcac	gtta	180	
gtggctgaaa	tgcgat	gccc	tgt	caaaaa	tagtactacg	aaag	ttt	gtt	accttagcgc	240	
gcatgaaaag	acc	aatctgt	ttt	atctct	gtcggtgatc	ttt	atcacc	gtt	tttatg	300	
actgcctgt	cacaga	agtc	caagac	gaac	aaactacc	aag	agatc	gg	agcc	caatg	360
agtatgtaca	gtcgat	ggat	gtg	cttagca	attt	atcggt	aac	gtcagg	ct	tgtat	420
cgataccata	agtat	caa	aac	aatgactcg	cgtgg	tatag	atgc	atgtt	ggg	ccccgtt	480
gaccctt	cgaat	acatt	cctt	acgagg	aaatggat	actg	aaat	ttt	atgacta	cgg	540
agagtatgcc	ggagt	cgag	ctat	catatc	gcagc	cccc	gat	atgcgt	gattat	ccag	600
agacctatgg	aagg	tatg	cc	cgcag	acgaa	gcagg	atg	aggc	gcac	cgcat	705
ctatcgatgg	gaa	agacttc	cgca	aaaccac	cac	accgaaa	gt	aa	gta	ag	

(2) INFORMATION FOR SEQ ID NO:17

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 854 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...854

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17

ccattgaaag	gcaatccgag	at	tttt	tgagt	gtaa	agt	tcgg	gcaat	actcg	ttgt	gtgcca	60
tatccagcgt	ataggtagaa	gtt	tgattat	ggcc	cactcg	aata	agggt	gcgtata	actc	ttt	gtat	120
tgtcggtgtt	tttactgaca	cg	tttccatc	ttt	ccatt	catc	ctt	ttt	gtt	gtt	gtat	180
gaaaatctat	accacatgt	ta	gt	tcg	cctt	ccg	agag	agt	gaga	acgt	tct	240
ccaccgatag	ttg	ctgt	ctac	cg	cccc	gg	aaac	ttt	ttt	ttt	ttt	300
tcgtccgcag	tag	ct	c	tc	ttt	ttt	ttt	ttt	ttt	ttt	ttt	360
tgtcgctatt	gaact	gt	act	gt	atc	ttt	ttt	ttt	ttt	ttt	ttt	420
gctgttgggg	acgata	act	gt	tc	ttt	ttt	ttt	ttt	ttt	ttt	ttt	480
gggtctgtcg	attt	actt	ttt	at	gt	ttt	ttt	ttt	ttt	ttt	ttt	540
ccactgttgc	gt	g	ct	tc	ttt	ttt	ttt	ttt	ttt	ttt	ttt	600
tgattagtg	cca	at	tg	at	ttt	ttt	ttt	ttt	ttt	ttt	ttt	660
tagatgaaag	ttt	cc	at	cc	ttt	ttt	ttt	ttt	ttt	ttt	ttt	720
tcaagatttg	att	gc	tt	tc	ttt	ttt	ttt	ttt	ttt	ttt	ttt	780
cacttatac	tcgg	tt	tc	tt	tc	ttt	ttt	ttt	ttt	ttt	ttt	840
cagcggagat	ct	g	at	tc	ttt	ttt	ttt	ttt	ttt	ttt	ttt	854

(2) INFORMATION FOR SEQ ID NO:18

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1162 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1162

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18

cgagacttcc	attccccccg	atttatatgg	ataagaagaa	cgccattgtt	attccgatga	60
tacagtctac	attcaaagcc	nggacaaaat	actccgagga	cgtctttca	ctgcaactca	120
agatatgggt	gagtaaccca	tattcaacat	tccggcgact	tactatgtga	gtgaagagga	180
ggacaaatcc	gccgaccat	accgattcg	caaggggatc	ggacagcaaa	gcctgcccgt	240
tctccttcat	gccgagacca	tcggttctc	caaccaccaa	agagcaaaaa	tgaataacctg	300
tacatactga	ttacactttt	actctccggc	ttttttccg	gtgtgagatt	gcttccttt	360
cttcggacaa	actgcgtctt	gagttggaca	ggatagaggc	gatctcacag	gcagagcgtt	420
aaacttgctg	tatcgacatc	cgaccaactg	gtgactactc	tccttgggg	taataatatc	480
gttttggtag	ctatggtctg	ctgatggcgg	gattgctggc	cgcaccttg	gcgcaatggt	540
tgataacgtat	gctatgatcg	tcgttctcca	atctgtctta	tccactatata	catactgttt	600
accggggaaat	ttctacccaa	agccattttc	aagaccatgc	caatatgtat	atgagggtat	660
tcgcccctccc	tatcgtagcg	atctatatact	gctttatcct	ctgtctaaac	tcttcaccgg	720
tttatctcgc	tctttattcg	tctgggtggac	aagaattatg	tgcctacaaac	agttagggttg	780
ggggccgtaga	tctcgatcat	tatggcag	aaaatatgtc	cggagaaaaac	gaaagaacga	840
cttgactacc	gaagtgaaaa	tcatccgaaa	tgcgtggat	tttccggat	tcaggtgcga	900
gactgcatga	tcccacgc	ttagatgata	gatgtgagtt	gcaaaacggat	atngaagtac	960
tcaaaaacgac	tttatcgat	ccggtttgtc	caagatcatt	atctacagac	agancataga	1020
tgacgttagt	gatataatcca	ttcgagcga	atgtttcg	ggcaagactg	gcaaaaacta	1080
tcaatactac	tgtattcgta	cccgaaaagc	atgtatgcca	ataaaactatg	cgactactca	1140
tgcagcgcaa	gaaaagcatt	gc				1162

(2) INFORMATION FOR SEQ ID NO:19

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 584 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...584

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19

gggaaggcat	tttctctgt	ttcgatgcgt	ttgcaggaac	catcagcacc	aaaactacag	60
atataacatc	gaagcgta	ccgagatcga	tggcgacta	cgcacatagt	gatgcgcaga	120
ttcggaaatc	agtcggcg	cttgcgtctc	acagcctt	cgggggccag	tagaaaggcct	180
tccgtacgag	tcttgcattcc	acaacgacca	gttctctgg	cgtggatgcc	acgatatacca	240
gctcgagcc	ccccgactgc	cagttcagg	cttctatctg	atagccttc	tgccgagg	300
tttcagcgc	atctcttcgc	cttggcg	cggtcgta	tgacggccat	tgcatactgtc	360
gagacctttt	ttttcggtcc	ggctgaggat	gagctctct	tgtgccgtt	tttttctct	420
tccaggatct	tacccacagc	atgaatatgc	cggttcc	cacctctccg	aaagactcat	480
tcactgcagt	ccgaaaacac	gcatctccgg	agacaaagct	atataatgcac	ttacgagana	540
ggatattga	tacccagctt	gcgcacttct	atattgagag	tctt		584

(2) INFORMATION FOR SEQ ID NO:20

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 964 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...964
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20

gggtctggaa	cgtctcacct	cgttagcgga	gctttatctt	ttggataaca	aatccgtaag	60
ctggagggtc	tggaacgtct	cacgtccctt	gcaacgctga	actatcggtt	aaccaaatcc	120
gtaagctgga	gggtctggaa	cgtctcagtc	cttagacaacg	cttgaactat	cgggttaacca	180
aatccgtaaa	ctagagggtct	ggaacgtctc	acttcgtttaa	caaagcttcg	tctaagaagt	240
aaccaatcag	taaactatag	ggcctggata	gtctcacctc	gctaacaaaa	cttttctctc	300
cgataaccaa	atcgttaaagc	tagagggtct	ggaacgtctc	ccccgtttagc	ggagctttat	360
cttttggata	acccaaatcag	taaactatagag	ggctgaaacg	tctcacgtcc	ttagcaacgc	420
ttgaactatc	gggttaaccaa	accgttaagct	ggagggtctg	gaacgtctca	cgtccttagc	480
aacgcttgaa	tatcggttaa	ccaaatccgt	aagctagagg	gtctggaaacg	tctcaattct	540
taacaaagct	tcgtctaaaga	agtaaccaa	tcaagttagct	agagggtcgg	aacgtctcac	600
gtccttagca	acgcttgaac	tatcggttaa	ccaaatcgta	agctggagggg	tctgaaacgt	660
ctcacgtct	tagcaacgct	tgaacttcg	gtaaccaa	cagtaagcta	gagggctctgg	720
aacgctctc	ttcgttaacaa	agcttcgtct	aagaagtaac	cagatcaga	aactagaggg	780
cctgaacgtc	tcacacctcgct	aacaaaactt	tctctctccg	ataaccaa	cagaagctag	840
agggtctgga	acgtctcacc	tcgttagcgg	agctttagtct	ttggataacc	aaatccgtaa	900
gcctggaggg	cctggAACGG	tcttacctng	tacaaagctt	tcgtctaaaga	agtacccaaa	960
tcag						964

(2) INFORMATION FOR SEQ ID NO:21

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 860 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...860
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:21

ggatccccctc	ttcgatctca	acgaatacac	cgaaattgggt	gaagttgcga	cacgagcatg	60
gtgacgagag	cctacaggg	aacgagttt	gatatcagcc	aggatccgg	tttgagttgc	120
ttcagaccga	gcgcacatttt	gcgttctcgc	ggtcgagcgt	caggatcacg	gcttccactt	180
cgtcgcctac	atgcagaagt	cctgagcaga	acgcaagtgc	tgtgtccatg	acatttcgct	240

acgtgataa	gaccctcaac	gccctgtca	atctcaacga	aagcaccgta	atctccatca	300
ccacaactt	acccttcacc	ttatcgccta	ccttaagctc	gcttcgagag	catcccaagg	360
tgaggcata	agctgtttga	gtccgagagc	gaacgcttgc	gatcttcattc	aaagtgcagg	420
ataacgacat	tgatcttctg	accagctgta	cgatttcttc	cgatgagcc	acacgacccc	480
atgaaaggctc	gtgatatgga	taagaccatc	caactccaccc	aggtcgataa	atactccgta	540
gaagtaatat	tcttgacgat	accttcgagt	acctgcctt	tttcgagctg	ccgatgattt	600
ctttcttctg	ttgttcgagc	tctgcttcga	tgagcaactt	tggaaacaa	ctacattctt	660
atattcttga	ttgattttca	caatctgaac	tccatcgatc	tctcaacgaa	tgcacatcgtag	720
tcgcgaatgg	ggcgcgcgtcg	atctgtgatc	ccgggaggaa	agcctcgata	ccgaatacat	780
cgacatcata	ccacccttgg	tacgacactt	cacatagccc	tttacgattt	cgtttttcg	840
agagcctcg	tcacgcgctc					860

(2) INFORMATION FOR SEQ ID NO:22

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 561 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...561

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22

ggttaccaat	ctcaccggaa	ctgcttccaa	tgacgaagtt	tctttggacg	ggacgggttg	60
gaagagaaag	ctgaagagcc	ggcaagtat	aaagcagtag	ctacaacgtc	tacaagaatg	120
gaaccttgc	cgtaataaca	gtgaaatca	ttatgtggag	accgggttag	ccaatggtag	180
atacatctac	gaagtggat	aaagtatct	gacgtgtat	ctccgaaggt	ggctgttaacc	240
gtgacgtgac	caacagctca	ttgagcaatg	tagatggaca	ggctccttac	acatgcgagt	300
agaaggcgaag	aaagattattg	cggaagccca	tggatgatc	acgtctacga	catcaacgga	360
cgtaccgtgg	ccgtagcccc	gaatcgattt	gatacatggc	gcaaaccggt	ttctatgcag	420
tgcgttgc	tgtggaaat	aacaccatgt	atcgaaaata	caagtaagat	aaagcagata	480
tttccccctg	ctaaagacaa	agaggctg	tcgagattat	tttcgatgc	agcctcttct	540
tttgctactc	atgcccgtat	t				561

(2) INFORMATION FOR SEQ ID NO:23

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 623 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...623

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23

gaactcacgt	taaaagtagat	tatagaaaaga	cccagtaacc	caattgtaga	ctatccggc	60
ccaactggc	aactttttc	agtagacacgnt	caaacttgc	gttggcgcg	ggagcgaaaa	120
aattctacg	ccactgcgaa	aaaattccgc	gcccgtttc	gggaaaacac	gcgcacaat	180
cggagcgtt	ctgggtgtat	ttccgaggct	gtcagggtga	gactttccga	caatgggtga	240
gctctactcc	tccatcctac	aggctcggcc	aacagacaag	cacgacatcc	ccaccattgc	300
cctcgcata	gactgtatgag	atcgtgactg	ttgatgcagg	aaccataaaa	aggaattttt	360
ttcggattca	tttggcgcat	aacaaaaaaa	gctaccttg	cagcgtcaaa	atcagaagga	420
gcttccttt	tgtgggtat	tactccgtag	ctcagggtgt	agagcaaatg	actcttaatc	480
atggggtcgt	agttcgagcc	tcaccggggt	cacaaccaa	tagcagaggg	ctgtgttgaa	540
tagtttttt	gacacgccc	ttaactttt	ggatcggggt	tcgcctttgt	gaaaggatat	600
ggaaaatatac	tgtcaaatgc	cga				623

(2) INFORMATION FOR SEQ ID NO:24

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 848 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...848

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24

ggccgaagcc	cagtacaata	tggctcgcaa	cggtgccgaa	cgcgaagaca	gctggcagct	60
tctgcctcg	tcgatagagc	gagaggagcc	gtcgccgagt	ggagtctgtac	atcaacgaaa	120
cctacctcat	cggcccacgg	gcagggcgagt	gtcggagata	ttccccaaag	ccggcgaact	180
cgtaggtacc	ggcgcactat	catgaatatc	gccgagatgg	gcgatatgtg	ggccagctt	240
gccgtcgta	ggatttctc	agcagcatga	ccatgggagc	cgttctggag	actgggtgcc	300
ggctctgaat	gaagaaaaag	tacgcttcaa	gatcacattc	atcagaacat	gggtacctat	360
gctgcctgga	aagcgaccaa	gacaacaggg	catacgacct	gaagacacctc	gaggtaaagg	420
ccacccttgc	ggataaagac	aggcacaaaa	gctacgccc	gttatgtccg	tgatcatacg	480
caagtaacga	gagcagtaag	gcatgcacg	ggacagccct	tatagccacc	atgcgtagaa	540
ggtgcgacaa	ctgacgagtc	ggtcctctt	cctcttctgc	atggtgatgc	tcctgtctt	600
tgctgtctct	tcttccctc	catcatggat	atggggtgcc	gcagaacctg	cctgcgggta	660
ttgtggatct	cgatcgatca	cagacgcgcg	caccatagca	cgccacctca	attcgatgga	720
gcaaacccaa	atcgtaaaca	gttcgaaggc	tgcgtgaggc	tcgcttgca	tacagcgagg	780
cgagtatcgt	actactatat	acccgaggaa	tgacacggat	gcctacgcac	agagcagcca	840
agctctct						848

(2) INFORMATION FOR SEQ ID NO:25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1866 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...1866

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25

ggcggcgaag	tagtccgaag	ccgaggggat	accgctcgct	cctccgtaaa	aatctccgaa	60
ggcaggtcg	ctccgcttcg	ggtcatttcg	tcgagaatc	atcgatgagc	gagaaggcgt	120
ccggctcctt	ttcgcccgag	gccccgttcag	ctgctccgga	tgcgtatatt	gctccacagg	180
caggtagcgc	ttgcgtgtc	cgcagatacg	ggtgcagcc	ggcgcagctc	cgaagcatag	240
cgcactcctg	caccacatac	atattatata	ggtataggaa	gacgaagggt	gagcgttaggg	300
ataggcctcg	tacaggcctt	tcatctcggg	cagcgtgtca	gccaaagccg	cgaggggtgc	360
tccatgttagg	cgtacagatac	gttagtcgtc	atgtggggga	ggattaccag	ttctctaccg	420
tagcgttata	cacctgcttc	acaagtcgtc	gaccatattg	gccagcaggg	cgtcttgtac	480
gtcaccaggc	gctcgctgct	gtcgaagtcc	gtggaaagacg	taaagtccc	atcgaagttt	540
gttcgggagg	ccttgttctc	gttagtgaccc	tgtatggata	aggttaccc	gtgcgtgcgg	600
ccagatcggt	gtcctgtacg	gcgaggggag	cgaagtctaa	ttagtgtatga	ccacctcgat	660
gatcatgtcg	gcatcggtgg	ttcgtgcatt	tgcagcttgg	tacggcgcgt	aaaatggttt	720
tggagggctt	cggcttagtc	tgcccaacg	ggggatatac	gcgggtggcc	tgattgtca	780
catccgcata	taaagcggtt	tgatgcggct	atagtccaga	gcacccctgt	tgagctgttag	840
gagatgctgc	atgccgagca	gttcagcagg	acgataagca	ccccgcaaga	gcggaaaggc	900
tgtatcgccc	gagggttcta	ttccagtcct	tctccttgcatt	tttacggat	agtgtccgct	960
ccgaaatctt	cagttcctcg	ctgtctgcct	gcgccttccg	ccgtggcggt	ccaatgcgaa	1020
gaaatcatt	tcttctctac	ctccctccagc	gaaaccggat	cctcggtgt	ttcgtctgggt	1080
cctgtatcggt	ctccacgggt	tctgcccgcgt	tcgcgtatggg	ggccttgcgt	tgctgacgccc	1140
ccacttcgg	tctgcgggtgc	gcttgcgtgc	gttgcggcaga	cgtccgaccc	tacaggccat	1200
gagggtctgtt	cgtgggtgcgc	caggcggttca	tcatccccctt	caaatcgct	atctctttct	1260
tcatatcgta	tagccctgg	agatgatttc	gchgctcgtaa	tgggggattt	gtttgtccgc	1320
ttcgtcggtt	cgttccgtcg	gatcacgacg	gggtggaggt	cttcgcattcc	ctagcgtcca	1380
ggttagcgagt	gatggttctc	gccgataccg	tccgcgttcc	cccaggatgc	tcagcctgtc	1440
ggttatattg	cgcagcttc	gcacattggc	ggccagcgggt	aacgcattaa	tatggtacgg	1500
gcttcgtccg	ataggcgcac	ggaggcgtac	gatacttctc	ggcgctgtcg	gcggcgaatc	1560
ggcgaaaagc	aagggcacgt	cgtccgggtcg	catacgcacg	gcaggcacct	cgatcgacc	1620
gtattgagcc	ggaagaagag	gtcttccgg	aacttcccgt	tgcgtacgcc	tccttggaggt	1680
tcacatcggt	cggcgtctacg	atacgacat	ccgtctctgc	gactggctgg	ctcttacggg	1740
gatgaactcg	cccggtctcca	gcacccgtac	agcctcgct	gcgtgggcaa	aaggcagttc	1800
gcccaactcg	tccgaaagaa	tcgtccggcc	ggatggcttc	ttcgaagttac	cccttgcgat	1860
ccgata						1866

(2) INFORMATION FOR SEQ ID NO:26

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 632 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...632

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26

cgaacagct	gaagcattgt	ccgtacgtct	tcgtttggc	attcgcccta	tcacgttctt	60
tgaagagttg	ctctgctcg	gc当地	cggcgagtg	gaacccactt	ctttttcat	120
cgctccttg	gc当地	gtgtcagtga	c当地	gagcctctt	gatgtcgagc	180
atacgtcca	acttactttg	tcgaggctgt	caaaaaggttc	atttgtttt	atgacctgca	240
tgtttttag	caatttagtga	tgaataacaa	c当地	gcttatcaaa	agctattgtg	300
gaggatatac	cactttcgta	aatataacaa	tctcagaata	tattttggtc	t当地	360
tcgaggaaaa	aagtgcata	gctcattacg	cccaaggcagg	atacgagcc	gaaatgctcc	420
gatttgtgtc	tgtgtttgt	gaaagcaggc	gcgagat	tttgc当地	gttca	480
t当地	cacgc当地	gaaaaggtt	cacgtgccac	acttttgggt	gtcataaacc	540
gaaaatttag	gcgtgtgaac	ccaatcgat	agggatgata	c当地	tgaatcgaa	600
gtgaatatgg	tgcaaaaaaa	gaggacagt	gc			632

(2) INFORMATION FOR SEQ ID NO:27

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2331 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...2331

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27

gcagatgcta	c当地	agactttgt	gtc当地	g	gaaagaatc	60
atcttcaat	tttggactgg	ttcagcactg	catcttattc	ggtgtagaaa	aaccagggtt	120
atgaaggctt	taccctgaaa	atgtcaaga	aatccggaa	ggatgtatg	aagccaaaga	180
cttctccgt	c当地	aggattcaaa	gacttgc当地	t当地	acctttcg	240
aacgact	caaggaatg	ccggatgaat	t当地	catattgaaa	gaatcgatgg	300
ccgaagcgt	t当地	aaacttctca	ttgggtat	gacaagacgg	taatcagg	360
gaggaaaaaa	tttgc当地	ggatgaaaatg	gatcggagg	aaccaagaaa	gtcatagagc	420
ttttagggccc	tttgc当地	aattgaaaaga	aggttctgtt	ttgctgatag	acgaattaga	480
tgccaaactc	acccccttt	gaccagaatg	attctgaatg	tg	tccggagaca	540
atcccaatgg	agcacagtt	atcttata	ctcacgacac	aaatctgcga	agggcgatta	600
tttacgc当地	gatcaa	atct	ggttacgg	aaaagacgg	c当地	660
tcattgatag	agttc当地	tgca	aggagg	t当地	cgatctt	720
acgactat	taacgacgtt	atggagctat	cccgtt	tttcaagtg	tagagccatg	780
ggacaccacc	aaaaagagaa	atagaacgac	taaaacgt	aaagcgagaa	gcaaaagccgc	840
aagaaaacgc	aaagagaata	cccggacat	aatagttcg	ttctgatcg	ttgtgaagga	900
caaaaagacgg	aaccaacta	ttttaaggct	tgattgacaa	ccactactcg	gaagttcgt	960
aggcagagat	tagggacaa	gttgttctac	ttgtgcatta	gtc当地	ccaaagagat	1020
tc当地	tc当地	gc当地	gc当地	ggat	tttgggt	1080
aagacgattt	t当地	atcaagct	tc当地	aaagagcatg	tttgc当地	1140
cgcttggaca	aacgaagctt	ttgat	gttctctcc	atttccaata	tctgatgt	1200
cctatcagcc	gtgatgctt	catt	ttgaaaactt	gata	cgacttaatg	1260
ataattctt	ccgaaacaata	agaatgtac	ctcctt	aaat	aaagccatgg	1320
agaggaattt	tagcaaagcg	at	aaacttcgt	t当地	ggtaaagat	1380
atgtcaatca	caacccctgt	acaagggtcg	atctt	taggaaatgg	aaaatcccct	1440
gtccgttata	aagaacaaat	aaagagggt	atcact	ccg	acttgaactc	1500
ctaattgtacg	tatagctt	gattgt	c当地	gg	gt	1560
tctcagggtt	caaattata	aggaaagaga	ctgaaaattt	ccaaaagaga	tc当地	1620
ctccctgacg	gactgcaatt	tat	tttgc当地	acgtt	ttgcaactat	1680
ttcaaaacaga	tgagagaaa	catttggcag	atacttcgt	ttc当地	tttctt	1740
ggacagcgt	cg	gacaggct	cagatcgaa	ccgtacata	gaggctt	1800
cgccgacgaa	gcttccgaca	gatgagccgc	tacaatatac	cg	ca	1860
cagcttgg	ggagacagga	gccggagcca	gtacactggc	cagcgt	acac	1920

gggatcaa	tgccacaaat	cgtggacggg	caagcgcacc	atcgtaaccga	cgatgcggc	1980
aacgaatgt	tccgcagcta	ttcggccg	gcgaatcgta	tgaagatcat	tcccgtt	2040
jctccaacc	acgctatctc	ccctgttcaa	actcgacaga	gaagactatc	ggggctggc	2100
cacggggtgc	aacgctgtgg	ctatgccacc	aatcggggct	atgccaatct	gctgataaga	2160
tggtggagct	gtatgagcta	tatgtttgg	atcgcgagaa	gtaccctcat	gttccacaa	2220
gtcttaccc	gggtccaaca	aaaaatccca	tcaacgacca	agcagaagca	gagcggactc	2280
aagcacgaag	cttacttcaa	gctccggact	ggctctacat	cataagccaa	g	2331

(2) INFORMATION FOR SEQ ID NO:28

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 784 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...784

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28

gcgtacgacc	ctttcgatgg	ggcataaaca	acgaaagaaa	acgagacaaa	acaaaaaacg	60
aatatagaat	tatgggaaa	atcattggaa	ttgacttagc	acaacgaact	cttgtgtctc	120
tgtattggaa	ggtaacgaac	ctatcgatt	acaaacagtg	agggcaagcg	cacaacgccc	180
tcggtatgg	cttttggat	ggtggcgagc	gtaaggtggg	cgatccggcc	aagcgtcagg	240
ccatcccaat	ccgaccaaga	cgatatactc	tatcaaacgc	ttcatggcg	aaactacat	300
caggttcca	gagaagtgg	gagagtgc	ttcaaggtag	tactggggac	aataatactc	360
cgcgcgtaga	tatagacggt	cgtctctata	cgcgcaggaa	atttcggcca	tgatccttca	420
gaagatgaag	aagacggccg	agactacctc	ggtcaggaag	taacggaggc	cgtgatcact	480
gtgcccgc	catcttacgc	gctcaacgtc	aggcaacgaa	agaagcagga	gagatcgccg	540
cctgaaaagtt	cgccgtattt	tgaacgagcc	tacggcagct	tctctggct	cggtctggac	600
aagtccata	aggatatgaa	gatcgctgtc	ttcgactggg	tggcggtacc	ttcgatatct	660
ctatcttgg	attggggc	ggcgtttcg	agtggaaatcg	accaacgtg	atacgcac	720
cgaggagac	gacttgacca	cgtgatcatt	gctggctggc	agaagagtca	agtctcaaga	780
agg						784

(2) INFORMATION FOR SEQ ID NO:29

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 545 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...545

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29

gcgagttac ggaagtaggt gctgatatcg aagttcaggt aatcgagatg acaaggaaaa	60
ccgtcgctc agctgggtc acaaacagtt ggaagagatc ctgggatgt attcgagacg	120
gtattcactg taggatctat ccacgaagaa cggtaatcga agtgatggac aagggtgctg	180
tcgttctct gccttagtg tgaaaggaaa tgccactccg aagcacatgg tgaaggaaga	240
tggctacagg ctgtactcga agagaagttt ctttcaagg ttattgagtt caataggatg	300
ccaagcgaat cattgtatct catagccgtg tattcgaaga tgacagaaaaa tggctcagcg	360
tgaagccaat gcagagcgtt aggctgaagc caagcggctc agaaaagaagc tgctggcaa	420
gctgccaatc ctgcacagggc ttagagaaaag ccactctcgg agacccggc gagctggccg	480
ctttgaagaa gcttcagaaa ctaaaactac tacggatcat acgcgccttg gcgtatgatc	540
actta	545

(2) INFORMATION FOR SEQ ID NO:30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 849 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...849

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30

gcctgtatct gttcgctgctg tgctcctttg agagccttgg cgttctgagc tttgcagctg	60
cttcggcagc ctttgcctgc tccatcttag ccgtacgcg ggggcttcga tgacagcggag	120
ggtatcgccg gcctgcaccc tctgtcctcg gataccctaa gttccttgcgat ggcggccggc	180
actttgctgg acactcgat tccgtcactt ctatctgtcc ttggataatc tcctcgccg	240
gtctggcatg aaaaaaccaa cgtacgtcac cactgcgtatg actcccgacca agagagaaac	300
gccgggaata cgatattacg ttgtttgttgc tccgtcataa tgaaatatgt ttgtatcagat	360
gaataacgaa ataaggaaaa acgttatcat tcgaaacgac ttcttccggg gagaggtgtc	420
ccgaaaggctt ggcgcgcatttccatcattcgatccgtcgatccgtcgatccgtcgatccgtcgat	480
agaccggggcc acaaccatgc cgtctgagct tccagttacgt tggaggccgt tattacgcct	540
cgcggaaacc tacattggca tagcgcaggat tctcttcggc ttcttcctg tcttcgtggc	600
catgacaagt cgtttgtctg cttcccgatccatcattcgatccgtcgatccgtcgatccgtcgat	660
atgccttcgcgt gtcgtttggc aagttgtggg ctgcgtatgcg tgcctcggtt tggccgctc	720
ttacctttagt cgtgcctgccc cccagtgcca gataggaact ttgagcatca caccacatt	780
ccactacctc cgaattatttc tcgaaaccat tgaaagagga cggattagtc actaatagtt	840
tggcaacga	849

(2) INFORMATION FOR SEQ ID NO:31

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2843 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...2843

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31

tgggtacggg	caagaccact	ttcatcaaag	ccgtatgcga	ggagctgggg	tctcgacgt	60
tatcaatagt	cccaccttt	cgattatcaa	cgagtaccct	cggtatcagac	gggcgaactg	120
atctatcact	tcgactgcta	ccggtcaca	agatagaaga	ccccctgaat	ctgggtgtag	180
aagactattt	cgataggta	gtctctgctt	tatcaatgg	ccggagcttc	tggagccgat	240
actccgaacg	atacggttca	tgtccgaatc	gaagagctgg	aagacggcaa	gcgcggctta	300
cattctaattg	cctgctccga	tgtcggtcgt	cattcgggac	ttcatctcat	cctcttgc	360
atagtccgtc	tgggttcgt	actgactgtc	ctctctgtcc	ggattggcta	ctgagcagcc	420
gaggcgcacg	catttggatc	atgccttcgg	caagcgaggc	gcacgtatct	tctatattat	480
aataggagtg	ccttgcgtag	tgtcggtct	ttcgggctga	tcaaactctg	aaaagtgtct	540
gcagtaaat	cgtcatata	aaagagaccc	cccctgctca	gcctcatttc	gtatattcct	600
tataacctct	tcaaggggaa	acettctaccc	ttacgggtga	atcaatttca	gaccgatgga	660
ttacgaaata	gagaacaacc	atgcgcgt	attcgcagg	gaagtatcga	agtatatgc	720
ggctccatgt	tcaatgcgt	acggaagagc	tgctacgccc	tctcgggaga	gctaagatag	780
cgcgcagacg	gtggagatat	tcaagccgac	catcgatata	cgctacgacg	aaaggatgtc	840
gtttcgatg	acaagaatgc	tatcgcttcc	acccctgtgg	acattcgcc	aatatactgc	900
tgctatcctc	ccaagtggat	gtgggggaa	tgacgaagcc	cagttcttgc	atgagggtct	960
tgtggagta	gcccagcaat	ggccgtatcg	ggtgtcgcg	ttgtgtatcgc	cggttggac	1020
atggactttg	acgtcagcc	ttcggaccta	tgccgggctt	gtgtgtccata	gccgactcgt	1080
gaccaaagtt	catgcccgt	gtgtggatg	cggttttttgc	ggcagtttc	tttccgtcgt	1140
gtccaaggcg	atcagcaatg	gtgtggggc	gaactgacga	atacagtccc	ctctgcagaa	1200
cctgtacag	gaaatgcagt	tctccccaca	aacagaagaa	atccattcga	caatatgaat	1260
agcagacatc	tgacatcaca	atatttgcgg	gcctctccct	ctttgtactg	acattgggca	1320
gctctccgt	gccccacaag	atacgcgt	gactctcgcc	ggaaagctt	ttttcgccg	1380
tggatacaac	gttcggccga	atatacgcg	ctttgcattc	agcatacaac	atcgctacgg	1440
aaagagtgg	cgctctacc	gcagaacgt	acaaggagat	aggccttatg	ccatcgtaac	1500
ggacatagac	gaaaccattt	tgacaatac	gcctaactcc	gtgttatcgg	ctcttaagg	1560
caagattaga	tgaagagact	tggggaaat	gggtgtcaca	gccccatgcc	gacacacggc	1620
aggagctttg	tctttcttcc	tccatgcgc	gaacaagggg	atcgatgtt	ttacgtcacc	1680
aaccgcagag	acaatctgcg	cgaaagcaact	tttcaaccc	tcagcggtac	ggattccct	1740
ttgccgatga	agaacatttgc	tttagaccc	ttggccatcc	gacaaagaac	cccgccgct	1800
caaaatacaa	gaaagtatga	aatagtatttgc	ctcataggag	acaacttgg	cgacttccac	1860
cattcttcaa	tacgaaagaa	gagtccggac	gcaaacaggc	tctgggcctt	aaggccgggaa	1920
gttggccgg	cacttcatc	tgctggccaa	tcccaactac	gatcttgg	accggcatgg	1980
tacggccgg	agtatccgc	actggccgaa	gagacaaagc	acttaaaca	ctgcactcac	2040
agacacgcag	atagcttca	acaaaacaca	tcgaatagac	agactcacac	tatggacaac	2100
aaacgacaag	caaaatagaa	agactgctcc	agaaagaact	cagcgagata	ttctggggaa	2160
tgcgaaatcc	ctggccggcg	taatagtttgc	ggtaacgaac	gtacggtaag	tcccgacctc	2220
agcatcgac	gtatacaccc	gagtatattc	ccatcgagaa	gagcagcgg	atttttgaga	2280
gcatcaaaaca	caatacaaag	acgtccgtt	tgacccgg	cagcaagg	gtacccaaact	2340
gcgcgaagata	ccgatttgac	attctacata	gatgactctc	tggattatct	ggagaatata	2400
gccgttgct	caatcaataa	gaaaacggcg	ctctctatca	agacgctgt	acttccctt	2460
tttcatagcc	cgccgttact	ttttctcccg	caaaagatta	gtgcggtaa	tgtgttttgc	2520
ctcggtttag	cgatagctgt	ctgcgtgg	ttccggcctt	ggtttgatc	ctctctattt	2580
tcaatgggt	cgaagcttgc	tcatgacgc	ttcggcagta	acggatcccc	ctcttatgat	2640
tcgttgcag	acaattcgct	gataaaggca	gatgataaaa	ctctgctcac	agctccgaa	2700
cggaagggtat	cggttgcgtac	agctttatcc	tcaccggaga	aggtttgtaa	agacgaagta	2760
tcgacagcag	gctgttttcc	tcatgggtgt	ggagatcgct	atccccgcac	tgtgaagata	2820
gactccatcg	tctttgcagg	caa				2843

(2) INFORMATION FOR SEQ ID NO:32

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 881 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...881
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:32

tccaggacgg	atacgccgca	tagctccaa	ccatgcctct	gtgctgatcc	ggccgaagag	60
cggtaacgggc	aaagagttga	tagccgaagc	tctgcacctg	ggagcaaacg	agcctcagcc	120
ccattcgtca	aggtaattt	gggtgggttc	ccgaaagttt	gttcgaaagt	gagctgttcg	180
gacataagaa	aggagctta	ccaatgcttt	ttccgacagg	aaaggacggt	tcgagctggc	240
tgatgcggca	cgatcttct	ggacgaaata	ggcgaactac	cggtcggcaa	ccaataaaac	300
tgctgcgagt	gctacaggaa	cagacattcg	agccgttggg	cgaagcgtct	cccaccgagt	360
ggacatccgt	gtggtatcgg	ctacgaatgc	ttcttggagc	gaatggtagc	cgaaggacgt	420
ttcagagagg	acctctacta	tgaatcaacc	tgatacatct	gcatctgcct	ccgctgcgtg	480
agcgtcagga	gatatacagc	tgctgggtga	agccttcagt	gaagcctttg	cccaatcgac	540
ggattgcccc	atgcccgtt	gagtgcggaa	gctatgcgcac	gtatctgtcc	atgcccctac	600
cgggcaatgt	acgcgaactg	aaaaacgtag	tggagcgcacg	ctattgctct	cgggatcgag	660
agaaatcagt	gcccgggatg	tggctgcttc	ggttcgcagg	tgacggcagc	agaccactcc	720
gacgaacggg	cttgcggac	atggaggaag	ctgctatccg	agagacgctg	actaaataca	780
acggaacgtt	agtcgtgctg	cacgacccctt	gggattgagc	cggcaagctc	tttccggcga	840
atggagaaat	acggactgtg	atagtgtta	aaacagaatac	g		881

(2) INFORMATION FOR SEQ ID NO:33

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 630 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...630
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:33

cctctgcttc	ccgtacagcc	gtatgtgcca	aaagcgagaa	gcctgttaatt	cacctgcagc	60
atagacattt	ggcagggaag	tttgcattcct	ctcattagct	ttacaccttt	gccggcaagc	120
accaatccga	gcgactcgaa	tccttgcgca	cggggcgacg	tcccacactc	atcaggatac	180
gttcccttc	gatctttgc	tttcccttc	gtattttacc	gttacagctc	cgttgcgaac	240
cgatgtactt	tgtgcccggag	gtagaatttt	attccttctt	tttcatatgt	agcggtagca	300
tagtgcatt	ttcgggatcg	ataccgttga	gtatttccgg	cagatctcca	ccacgtgcac	360
ttgcgtaccg	ataccgttga	agaaaagaagc	gactccattc	cgtactcc	accacccatg	420
atgacgagag	aggtcgaaat	cctttgttct	gtagagcttc	acgggtttgtc	caatactctg	480
tctgctccac	ccggggatgg	gttgaataaa	cgtctccgaa	ccggtagatcata	gtacggatgt	540
gcagctttgt	actgtgcttc	gcccggatgaa	tgccgatgat	gccgtctgtat	cgcacccgt	600
acggtagctt	ctgcccgtcac	atctctactc				630

(1) INFORMATION FOR SEQ ID NO:34

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1353 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION 1...1353

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34

tcggcatttt	cggttcgaaa	atccaagttt	ccaaccaanc	cacagacttg	atcgctcccc	60
tttgcatagc	aaatctgtga	ctgcccgttc	atccggaaaca	ggaaactttt	ttcttggat	120
cgttcaagaa	cgnaaagtct	gtgcccacga	ttggcacaag	tccttcccg	cctgttagag	180
attgaggact	gtcagcaatc	ggactttcgc	atcggtcatt	atgacagacg	aggaagtatt	240
gaacaccgccc	aaacggtcat	tgttatgctt	aaagggataa	atccgaatcg	tgccacacgt	300
aattgcaata	cgtagttaga	gatggcatac	gactttacac	aaaattccgc	aacagcctgg	360
agtacagcta	tcaaggaagca	acccgtctcg	gctcgtagcc	gtgacgcgaag	atatgctcgt	420
actcggtatac	attcgcgacg	ggacaatggc	gcgatcgaca	tcatgcgcga	ctatgggatc	480
aacttgtacg	actcaaacgg	ttgatcgagt	tggaagccat	cgccgagagt	ttgcctgctc	540
gcctgaggga	tcgcccattct	tcaccccttc	ggctcggag	gctatcgaga	tgccacacagac	600
atctgtgccg	acatggagga	cgaggccgtc	agccggcca	tctgttgctg	agtatcctca	660
actcgacaca	ggagagctt	gtacaaagat	atttatgaaa	caaggataaa	aatacgacac	720
catcctgtcg	gattattcgg	acagcgcac	ccctccgaag	ggaagtctcc	ctccgaaatg	780
gagacctcga	cgggtaccaa	gacaacgact	tcgacgacga	agaggacaa	tccctccgccc	840
ttccggaaat	agcgggacag	gcggaggctc	cgcgacacg	ccgaacagaa	taccggcgga	900
ggcgatacta	ccaccacgac	acggagtgaa	gcgacacg	tgcactggac	acccctcgca	960
ccgacatcac	tgccatggcg	cagcaggcaa	gctcgaccc	gtagtgggtc	gggagcagga	1020
gatcgaaagg	tgatacagat	actcagccgg	cgcaaaaaga	acaatcccg	gctcatcg	1080
aacctcggt	atggcagag	tgccatcg	gaaggactgg	ccgaacgatc	gtgaaacagga	1140
aggtgagccg	tattttttc	gacaagcga	tcatcac	gattttggct	cagatggtag	1200
ccggcaccaa	atatcgcga	cagttgaga	gcccgtt	gcccgtctc	atgagctgaa	1260
gaagaatccg	cagacatnct	tttcatcgac	gagatacata	ccatcgtgg	gaagcaggct	1320
ctgagccgga	tcgatggata	ccgtcaat	at			1353

(2) INFORMATION FOR SEQ ID NO:35

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 467 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION 1...467

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35

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ccggagagag acgttttcc ttcgaaaaga taactgccat ccccaaaaac ttaaagggga 60
gttcttcctc atcgtaactcg tccgtaatct cgccgacgtc tttcccaat atgtcctcca 120
ttgtgatcag tccgcaagtg ccaccgactc atccacaacg atggagacat gcaccttatt 180
ggctctgaac tcctcgcaa atcatctatg cgcttgggg 240
cgaaatagagg atgccagtcg aattcatcgc ctttatccat gtgtgggatt agatttgat 300
gtaaatcacc ccttgatat tgtcttctga cccctctgaa acggaagtct ggaataaccc 360
gacgaaacaa cgaagtcaag catcttacga aaggccagct cagatccaca tccacaatat 420
cgatacgcgg gaaccatgga ttgcgaggct ggcttattat aggaatt 467

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(2) INFORMATION FOR SEQ ID NO:36

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 452 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- ii) MOLECULE TYPE: DNA (genomic)
- iii) HYPOTHETICAL: NO
- iv) ANTI-SENSE: UNKNOWN
- vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- ix) FEATURE:
 - (A) NAME/KEY: misc feature
 - (B) LOCATION 1...452

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36

gccataacctg	tccgattgg	gcggctgt	tc	ccaaacgc	gaatacaact	ccgcttgg	60
tgttagtactt	ggccgtag	tca	atttgtatc	cgccgtt	ggttagctg	gagtgc	120
tacaaggcc	ttgcctat	gc	tctttgtccc	atc	agtagtac	ccctgtcc	180
gctccggta	caatctcg	at	gaagatgc	gttgc	atgtccat	gatcaggact	240
gtttctgtcg	atcggtt	ca	aatgtgc	aaatac	ggac	actatcg	300
ttggtcgtta	ccacacctt	tt	gcctttagg	acgaa	acat	gactntg	360
gcatcagtcc	gccaccatt	tt	cttcttaaa	tcaaaat	tgatatct	caatcgac	420
nacgaagatc	caacaagg	cc	ggcgcac	tt	atc	gtttgt	452

(2) INFORMATION FOR SEQ ID NO:37

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1157 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- ii) MOLECULE TYPE: DNA (genomic)
- iii) HYPOTHETICAL: NO
- iv) ANTI-SENSE: UNKNOWN
- vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1157
- xi) SEQUENCE DESCRIPTION: SEQ ID NO:37

qtattgaagg	tcgtatccct	tggtcgctat	cacatccctt	ggcttcatcg	taaggacgag	60
;cgatccg	gcacgatgga	tgcgcgccaa	gacggcttaa	gctctatgtc	caccatccgg	120
cgaatctccg	tcttgcccag	ttggtcgaga	ggatgatatac	gtccaaacgg	ttgagaaatt	180
cggggctgaa	cgtctttca	gagctttttg	gatcacggaa	cggctatgtc	ccttgttcgc	240
ttcctgtctt	tttccgaacg	gaacccgata	ccctgcccga	agtctttgag	ctgggtgtac	300
ccacgttgg	ggtgatgatg	atcacgggt	tcttggaaatt	caccggcgtc	ccagactgtc	360
ggtcagctga	ccttcgtcca	tcacctgtaa	gacagattga	agacatccgc	atgcgccttt	420
tcgatctcat	ccaagagaac	ccggaatagg	gtttgcgtct	tacgcgcctc	gtcagttggc	480
cgccttcttc	tagcccacat	atccccggagg	ggcacccacg	agacgcgaaa	cggagaactc	540
tccatatact	cgctcatatc	caccctgatc	atggcattct	catcctcgac	aggtattcgg	600
cgagcttctt	ggccaaatag	gtttgccta	ccccctgggg	ccgaggaaaa	ggaaagaacc	660
gatcggtttc	tttcattgc	gaagtccaga	cgattgcgt	ggatggcatg	caccatcttt	720
tcgatggctg	tgtccgacct	actactttgg	tcttggatc	atctgcacatc	gtgcgcagac	780
gttcccttcg	cccggtctca	gccgctcagc	cggaacgcct	gtcatcaacg	ccatacatgc	840
gccactacat	tctcgccac	cgtctcgccg	tgcttggaca	tcgctcttcc	cattttttct	900
tctctccgc	tatctgctgc	ttagtgcgcc	gtcctgatcg	cggaaggagg	cagccagttc	960
gtagttctga	gccttacgg	cgagagctt	ttctctcgca	ccgatgccaa	ttcggcttcc	1020
agtatctcg	ttcttcgga	gccaccacat	tggtgatata	gacgctcgcg	ccggcctctc	1080
catggcatct	atgccttat	ctggaaagaa	acgatcgat	acatagcata	ggtcagttcc	1140
actgcccgtt	tgatcgc					1157

